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# Bayesian computing with INLA: new features

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## Abstract

The INLA approach for approximate Bayesian inference for latent Gaussian models has been shown to give fast and accurate estimates of posterior marginals and also to be a valuable tool in practice via the R-package R-INLA. In this paper we formalize new developments in the R-INLA package and show how these features greatly extend the scope of models that can be analyzed by this interface. We also discuss the current default method in R-INLA to approximate posterior marginals of the hyperparameters using only a modest number of evaluations of the joint posterior distribution of the hyperparameters, without any need for numerical integration.

**Keywords:** Approximate Bayesian inference, INLA, Latent Gaussian models

## 1 Introduction

The Integrated Nested Laplace Approximation (INLA) is an approach proposed by Rue et al. (2009) to perform approximate fully Bayesian inference on the class of latent Gaussian models (LGMs). INLA makes use of deterministic nested Laplace approximations and, as an algorithm tailored to the class of LGMs, it provides a faster and more accurate alternative to simulation-based MCMC schemes. This is demonstrated in a series of examples ranging from simple to complex models in Rue et al. (2009). Although the theory behind INLA has been well established in Rue et al. (2009), the INLA method continues to be a research area in active development. Designing a tool that allows the user the flexibility to define their own model with a relatively

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easy to use interface is an important factor for the success of any approximate inference method. The R package INLA, hereafter referred as R-INLA, provides this interface and allow users to specify and perform inference on complex LGMs.

The breadth of classical Bayesian problems covered under the LGM framework, and therefore handled by INLA, is — when coupled with the user-friendly R-INLA interface — a key element in the success of the INLA methodology. For example, INLA has been shown to work well with generalized linear mixed models (GLMM) (Fong et al., 2010), spatial GLMM (Eidsvik et al., 2009), Bayesian quantile additive mixed models (Yue and Rue, 2011), survival analysis (Martino et al., 2011b), stochastic volatility models (Martino et al., 2011a), generalized dynamic linear models (Ruiz-Cárdenas et al., 2011), change point models where data dependency is allowed within segments (Wyse et al., 2011), spatio-temporal disease mapping models (Schrödle and Held, 2011), models to complex spatial point pattern data that account for both local and global spatial behavior (Illian et al., 2011), and so on.

There has also been a considerable increase in the number of users that have found in INLA the possibility to fit models that they were otherwise unable to fit. More interestingly, those users come from areas that are sometimes completely unrelated to each other, such as econometrics, ecology, climate research, etc. Some examples are bi-variate meta-analysis of diagnostic studies (Paul et al., 2010), detection of under-reporting of cases in an evaluation of veterinary surveillance data (Schrödle et al., 2011), investigation of geographic determinants of reported human *Campylobacter* infections in Scotland (Bessell et al., 2010), the analysis of the impact of different social factors on the risk of acquiring infectious diseases in an urban setting (Willing et al., 2012), analysis of animal space use metrics (Johnson et al., 2011), animal models used in evolutionary biology and animal breeding to identify the genetic part of traits (Holand et al., 2011), analysis of the relation between biodiversity loss and disease transmission across a broad, heterogeneous ecoregion (Haas et al., 2011), identification of areas in Toronto where spatially varying social or environmental factors could be causing higher incidence of lupus than would be expected given the population (Li et al., 2011), and spatio-temporal modeling of particulate matter concentration in the North-Italian region Piemonte (Cameletti et al., 2012). The relative black-box format of INLA allows it to be embedded in external tools for a more integrated data analysis. For example, Beale et al. (2010) mention that INLA has been used by tools embedded in a Geographical Information System (GIS) to evaluate the spatial relationships between health and the environment data. The model selection measures available in INLA are also something very much appreciated in the applied work mentioned so far. Such quantities include marginal likelihood, deviance information criterion (DIC) (Spiegelhalter et al., 2002),

and other predictive measures.

Some extensions to the work of Rue et al. (2009) have also been presented in the literature; Hosseini et al. (2011) extends the INLA approach to fit spatial GLMM with skew normal priors for the latent variables instead of the more standard normal priors, Sørbye and Rue (2010) extend the use of INLA to joint inference and present an algorithm to derive analytical simultaneous credible bands for subsets of the latent field based on approximating the joint distribution of the subsets by multivariate Gaussian mixtures, Martins and Rue (2012) extend INLA to fit models where independent components of the latent field can have non-Gaussian distributions, and Cseke and Heskes (2011) discuss variations of the classic Laplace-approximation idea based on alternative Gaussian approximations (see also (Rue et al., 2009, pp. 386-7) for a discussion on this issue).

A lot of advances have been made in the area of spatial and spatial-temporal models, Eidsvik et al. (2011) address the issue of approximate Bayesian inference for large spatial datasets by combining the use of prediction process models as a reduced-rank spatial process to diminish the dimensionality of the model and the use of INLA to fit this reduced-rank models. INLA blends well with the work of Lindgren et al. (2011) where an explicit link between Gaussian Fields (GFs) and Gaussian Markov Random Fields (GMRFs) allow the modeling of spatio and spatio-temporal data to be done with continuously indexed GFs while the computations are carried out with GMRFs, using INLA as the inferential algorithm.

The INLA methodology requires some expertise in numerical methods and computer programming to be implemented, since all procedures required to perform INLA need to be carefully implemented to achieve a good speed. This can, at first, be considered a disadvantage when compared with other approximate methods such as (naive) MCMC schemes that are much easier to implement, at least on a case by case basis. To overcome this, the **R-INLA** package was developed to provide an easy to use interface to the stand-alone C coded *inla* program.<sup>1</sup> To download the package one only needs one line of **R** code that can be found on the download section of the INLA website (<http://www.r-inla.org/>). In addition, the website contains several worked out examples, papers and even the complete source code of the project.

In Rue et al. (2009) most of the attention was focused on the computation of the posterior marginal of the elements of the latent field since those are usually the biggest challenge when dealing with LGMs given the high dimension of the latent field usually found in models of interest. On the other hand, it was mentioned that the posterior marginal of the unknown parameters not in the latent field, hereafter refereed as hyperparameters, are obtained via nu-

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<sup>1</sup>The dependency on the stand-alone C program is the reason why **R-INLA** is not available on CRAN.

merical integration of an interpolant constructed from evaluations of the Laplace approximation of the joint posterior of the hyperparameters already computed in the computation of the posterior marginals of the latent field. However, details of such interpolant were not given. The first part of this paper will show how to construct this interpolant in a cost-effective way. Besides that, we will describe the algorithm currently in use in **R-INLA** package that completely bypass the need for numerical integration, providing accuracy and scalability.

Unfortunately, when an interface is designed, a compromise must be made between simplicity and generality, meaning that in order to build a simple to use interface, some models that could be handled by the INLA method might not be available through that interface, hence not available to the general user. The second part of this paper will formalize some new developments already implemented on the **R-INLA** package and show how these new features greatly extend the scope of models available through that interface. It is important to keep in mind the difference between the models that can be analyzed by the INLA method and the models that can be analyzed through the **R-INLA** package. The latter is contained within the first, which means that not every model that can be handled by the INLA method is available through the **R-INLA** interface. Therefore, this part of the paper will formalize tools that extend the scope of models within **R-INLA** that were already available within the theoretical framework of the INLA method.

Section 2 will present an overview of the latent Gaussian models and of the INLA methodology. Section 3 will address the issue of computing the posterior marginal of the hyperparameters using a novel approach. A number of new features already implemented in the **R-INLA** package will be formalized in Section 4 together with examples highlighting their usefulness.

## 2 Integrated Nested Laplace Approximation

In Section 2.1 we define latent Gaussian models using a hierarchical structure highlighting the assumptions required to be used within the INLA framework and point out which components of the model formulation will be made more flexible with the features presented in Section 4. Section 2.2 gives a brief description of the INLA approach and presents the task of approximating the posterior marginals of the hyperparameters that will be formalized in Section 3. A basic description of the **R-INLA** package is given in Section 2.3 and this is mainly to situate the reader when going through the extensions in Section 4.

## 2.1 Latent Gaussian models

The INLA framework was designed to deal with latent Gaussian models, where the observation (or response) variable  $y_i$  is assumed to belong to a distribution family (not necessarily part of the exponential family) where some parameter of the family  $\phi_i$  is linked to a structured additive predictor  $\eta_i$  through a link function  $g(\cdot)$ , so that  $g(\phi_i) = \eta_i$ . The structured additive predictor  $\eta_i$  accounts for effects of various covariates in an additive way:

$$\eta_i = \alpha + \sum_{j=1}^{n_f} f^{(j)}(u_{ji}) + \sum_{k=1}^{\eta_\beta} \beta_k z_{ki} + \epsilon_i, \quad (1)$$

where  $\{f^{(j)}(\cdot)\}$ 's are unknown functions of the covariates  $\mathbf{u}$ , used for example to relax linear relationship of covariates and to model temporal and/or spatial dependence, the  $\{\beta_k\}$ 's represent the linear effect of covariates  $\mathbf{z}$  and the  $\{\epsilon_i\}$ 's are unstructured terms. Then a Gaussian prior is assigned to  $\alpha$ ,  $\{f^{(j)}(\cdot)\}$ ,  $\{\beta_k\}$  and  $\{\epsilon_i\}$ .

We can also write the model described above using a hierarchical structure, where the first stage is formed by the likelihood function with conditional independence properties given the latent field  $\mathbf{x} = (\boldsymbol{\eta}, \alpha, \mathbf{f}, \boldsymbol{\beta})$  and possible hyperparameters  $\boldsymbol{\theta}_1$ , where each data point  $\{y_i, i = 1, \dots, n_d\}$  is connected to one element in the latent field  $x_i$ . Assuming that the elements of the latent field connected to the data points are positioned on the first  $n_d$  elements of  $\mathbf{x}$ , we have

$$\textbf{Stage 1. } \mathbf{y}|\mathbf{x}, \boldsymbol{\theta}_1 \sim \pi(\mathbf{y}|\mathbf{x}, \boldsymbol{\theta}_1) = \prod_{i=1}^{n_d} \pi(y_i|x_i, \boldsymbol{\theta}_1).$$

Two new features relaxing the assumptions of Stage 1 within the R-INLA package will be presented in Section 4. Section 4.1 will show how to fit models where different subsets of data come from different sources (i.e. different likelihoods) and Section 4.4 will show how to relax the assumption that each observation can only depend on one element of the latent field and allow it to depend on a linear combination of the elements in the latent field.

The conditional distribution of the latent field  $\mathbf{x}$  given some possible hyperparameters  $\boldsymbol{\theta}_2$  forms the second stage of the model and has a joint Gaussian distribution,

$$\textbf{Stage 2. } \mathbf{x}|\boldsymbol{\theta}_2 \sim \pi(\mathbf{x}|\boldsymbol{\theta}_2) = \mathcal{N}(\mathbf{x}; \boldsymbol{\mu}(\boldsymbol{\theta}_2), \mathbf{Q}^{-1}(\boldsymbol{\theta}_2)),$$

where  $\mathcal{N}(\cdot; \boldsymbol{\mu}, \mathbf{Q}^{-1})$  denotes a multivariate Gaussian distribution with mean vector  $\boldsymbol{\mu}$  and a precision matrix  $\mathbf{Q}$ . In most applications, the latent Gaussian field have conditional independence properties, which translates into a sparse precision matrix  $\mathbf{Q}(\boldsymbol{\theta}_2)$ , which is of extreme importance for the numerical algorithms that will follow. A multivariate Gaussian distribution with sparse precision matrix is known as a *Gaussian Markov Random Field* (GMRF) (Rue and Held,

2005). The latent field  $\mathbf{x}$  may have additional linear constraints of the form  $\mathbf{Ax} = \mathbf{e}$  for an  $k \times n$  matrix  $\mathbf{A}$  of rank  $k$ , where  $k$  is the number of constraints and  $n$  the size of the latent field. Stage 2 is very general and can accommodate an enormous number of latent field structures. Sections 4.2, 4.3 and 4.6 will formalize new features of the R-INLA package that gives the user greater flexibility to define these latent field structure, i.e. enable them to define complex latent fields from simpler GMRFs building blocks.

The hierarchical model is then completed with an appropriate prior distribution for the hyperparameters of the model  $\boldsymbol{\theta} = (\boldsymbol{\theta}_1, \boldsymbol{\theta}_2)$

**Stage 3.**  $\boldsymbol{\theta} \sim \pi(\boldsymbol{\theta})$ .

## 2.2 INLA methodology

For the hierarchical model described in Section 2.1, the joint posterior distribution of the unknowns then reads

$$\begin{aligned} \pi(\mathbf{x}, \boldsymbol{\theta} | \mathbf{y}) &\propto \pi(\boldsymbol{\theta}) \pi(\mathbf{x} | \boldsymbol{\theta}) \prod_{i=1}^{n_d} \pi(y_i | x_i, \boldsymbol{\theta}) \\ &\propto \pi(\boldsymbol{\theta}) |\mathbf{Q}(\boldsymbol{\theta})|^{n/2} \exp \left[ -\frac{1}{2} \mathbf{x}^T \mathbf{Q}(\boldsymbol{\theta}) \mathbf{x} + \sum_{i=1}^{n_d} \log\{\pi(y_i | x_i, \boldsymbol{\theta})\} \right] \end{aligned}$$

and the marginals of interest can be defined as

$$\begin{aligned} \pi(x_i | \mathbf{y}) &= \int \pi(x_i | \boldsymbol{\theta}, \mathbf{y}) \pi(\boldsymbol{\theta} | \mathbf{y}) d\boldsymbol{\theta} \quad i = 1, \dots, n \\ \pi(\boldsymbol{\theta}_j | \mathbf{y}) &= \int \pi(\boldsymbol{\theta} | \mathbf{y}) d\boldsymbol{\theta}_{-j} \quad j = 1, \dots, m \end{aligned}$$

while the approximated posterior marginals of interest  $\tilde{\pi}(x_i | \mathbf{y})$ ,  $i = 1, \dots, n$  and  $\tilde{\pi}(\boldsymbol{\theta}_j | \mathbf{y})$ ,  $j = 1, \dots, m$  returned by INLA has the following form

$$\tilde{\pi}(x_i | \mathbf{y}) = \sum_k \tilde{\pi}(x_i | \boldsymbol{\theta}^{(k)}, \mathbf{y}) \tilde{\pi}(\boldsymbol{\theta}^{(k)} | \mathbf{y}) \Delta \boldsymbol{\theta}^{(k)} \quad (2)$$

$$\tilde{\pi}(\boldsymbol{\theta}_j | \mathbf{y}) = \int \tilde{\pi}(\boldsymbol{\theta} | \mathbf{y}) d\boldsymbol{\theta}_{-j} \quad (3)$$

where  $\{\tilde{\pi}(\boldsymbol{\theta}^{(k)} | \mathbf{y})\}$  are the density values computed during a grid exploration on  $\tilde{\pi}(\boldsymbol{\theta} | \mathbf{y})$ .

Looking at [(2)-(3)], we can see that the method can be divided into three main tasks, firstly propose an approximation  $\tilde{\pi}(\boldsymbol{\theta} | \mathbf{y})$  to the joint posterior of the hyperparameters  $\pi(\boldsymbol{\theta} | \mathbf{y})$ , secondly propose an approximation  $\tilde{\pi}(x_i | \boldsymbol{\theta}, \mathbf{y})$  to the marginals of the conditional distribution of the latent field given the data and the hyperparameters  $\pi(x_i | \boldsymbol{\theta}, \mathbf{y})$  and finally explore  $\tilde{\pi}(\boldsymbol{\theta} | \mathbf{y})$  on a grid and use it to integrate out  $\boldsymbol{\theta}$  in Eq. (2) and  $\boldsymbol{\theta}_{-j}$  in Eq. (4).

Since we don't have  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  evaluated at all points required to compute the integral in Eq. (3) we construct an interpolation  $I(\boldsymbol{\theta}|\mathbf{y})$  using the density values  $\{\tilde{\pi}(\boldsymbol{\theta}^{(k)}|\mathbf{y})\}$  computed during the grid exploration on  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  and approximate (3) by

$$\tilde{\pi}(\boldsymbol{\theta}_j|\mathbf{y}) = \int I(\boldsymbol{\theta}|\mathbf{y}) d\boldsymbol{\theta}_{-j}. \quad (4)$$

Details on how to construct such interpolant were not given in Rue et al. (2009). Besides the description of the interpolation algorithm used to compute Eq. (4), Section 3 will present a novel approach to compute  $\tilde{\pi}(\boldsymbol{\theta}_j|\mathbf{y})$  that bypass numerical integration.

The approximation used for the joint posterior of the hyperparameters  $\pi(\boldsymbol{\theta}|\mathbf{y})$  is

$$\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y}) \propto \frac{\pi(\mathbf{x}, \boldsymbol{\theta}, \mathbf{y})}{\pi_G(\mathbf{x}|\boldsymbol{\theta}, \mathbf{y})} \Big|_{\mathbf{x}=\mathbf{x}^*(\boldsymbol{\theta})} \quad (5)$$

where  $\pi_G(\mathbf{x}|\boldsymbol{\theta}, \mathbf{y})$  is a Gaussian approximation to the full conditional of  $\mathbf{x}$  obtained by matching the modal configuration and the curvature at the mode, and  $\mathbf{x}^*(\boldsymbol{\theta})$  is the mode of the full conditional for  $\mathbf{x}$ , for a given  $\boldsymbol{\theta}$ . Expression (5) is equivalent to the Laplace approximation of a marginal posterior distribution (Tierney and Kadane, 1986), and it is exact if  $\pi(\mathbf{x}|\mathbf{y}, \boldsymbol{\theta})$  is a Gaussian.

For  $\pi(x_i|\boldsymbol{\theta}, \mathbf{y})$ , three options are available, and they vary in terms of speed and accuracy. The fastest option,  $\pi_G(x_i|\boldsymbol{\theta}, \mathbf{y})$ , is to use the marginals of the Gaussian approximation  $\pi_G(\mathbf{x}|\boldsymbol{\theta}, \mathbf{y})$  already computed when evaluating expression (5). The only extra cost to obtain  $\pi_G(x_i|\boldsymbol{\theta}, \mathbf{y})$  is to compute the marginal variances from the sparse precision matrix of  $\pi_G(\mathbf{x}|\boldsymbol{\theta}, \mathbf{y})$ , see Rue et al. (2009) for details. The Gaussian approximation often gives reasonable results, but there can be errors in the location and/or errors due to the lack of skewness (Rue and Martino, 2007). The more accurate approach would be to do again a Laplace approximation, denoted by  $\pi_{LA}(x_i|\boldsymbol{\theta}, \mathbf{y})$ , with a form similar to expression (5)

$$\pi_{LA}(x_i|\boldsymbol{\theta}, \mathbf{y}) \propto \frac{\pi(\mathbf{x}, \boldsymbol{\theta}, \mathbf{y})}{\pi_{GG}(\mathbf{x}_{-i}|x_i, \boldsymbol{\theta}, \mathbf{y})} \Big|_{\mathbf{x}_{-i}=\mathbf{x}_{-i}^*(x_i, \boldsymbol{\theta})}, \quad (6)$$

where  $\mathbf{x}_{-i}$  represents the vector  $\mathbf{x}$  with its  $i$ -th element excluded,  $\pi_{GG}(\mathbf{x}_{-i}|x_i, \boldsymbol{\theta}, \mathbf{y})$  is the Gaussian approximation to  $\mathbf{x}_{-i}|x_i, \boldsymbol{\theta}, \mathbf{y}$  and  $\mathbf{x}_{-i}^*(x_i, \boldsymbol{\theta})$  is the modal configuration. A third option  $\pi_{SLA}(x_i|\boldsymbol{\theta}, \mathbf{y})$ , called simplified Laplace approximation, is obtained by doing a Taylor expansion on the numerator and denominator of expression (6) up to third order, thus correcting the Gaussian approximation for location and skewness with a much lower cost when compared to  $\pi_{LA}(x_i|\boldsymbol{\theta}, \mathbf{y})$ . We refer to Rue et al. (2009) for a detailed description of the Gaussian, Laplace and simplified Laplace approximations to  $\pi(x_i|\boldsymbol{\theta}, \mathbf{y})$ .



### 2.3 R-INLA interface

In this Section we present the general structure of the R-INLA package since the reader will benefit from this when reading the extensions proposed in Section 4. The syntax for the R-INLA package is based on the built-in `glm` function in R, and a basic call starts with

```
formula = y ~ a + b + a:b + c*d + f(idx1, model1, ...) + f(idx2, model2, ...)
```

where `formula` describe the structured additive linear predictor described in Eq. (1). Here, `y` is the response variable, the term `a + b + a:b + c*d` hold similar meaning as in the built-in `glm` function in R and are then responsible for the fixed effects specification. The `f()` terms specify the general Gaussian random effects components of the model and represent the smooth functions  $\{f^{(j)}(\cdot)\}$  in Eq. (1). In this case we say that both `idx1` and `idx2` are latent building blocks that are combined together to form a joint latent Gaussian model of interest. Once the linear predictor is specified, a basic call to fit the model with R-INLA takes the following form:

```
result = inla(formula, data = data.frame(y, a, b, c, d, idx1, idx2),  
              family = "gaussian")
```

After the computations the variable `result` will hold an S3 object of class `"inla"`, from which summaries, plots, and posterior marginals can be obtained. We refer to the package website <http://www.r-inla.org> for more information about model components available to use inside the `f()` functions as well as more advanced arguments to be used within the `inla()` function.

## 3 On the posterior marginals for the hyperparameters

This Section starts by describing the grid exploration required to integrate out the uncertainty with respect to  $\theta$  when computing the posterior marginals of the latent field. It also presents two algorithms that can be used to compute the posterior marginals of the hyperparameters with little additional cost by using the points of the joint density of the hyperparameters already evaluated during the grid exploration.

### 3.1 Grid exploration

The main focus in Rue et al. (2009) lies on approximating posterior marginals for the latent field. In this context,  $\tilde{\pi}(\theta|\mathbf{y})$  is used to integrate out uncertainty with respect to  $\theta$  when approximating  $\tilde{\pi}(x_i|\mathbf{y})$ . For this task we do not need a detailed exploration of  $\tilde{\pi}(\theta|\mathbf{y})$  as long as we are able

to select good evaluation points for the numerical solution of Eq. (2). Rue et al. (2009) propose two different exploration schemes to perform the integration.

Both schemes require a reparametrization of  $\boldsymbol{\theta}$ -space in order to make the density more regular, we denote such parametrization as the  $\mathbf{z}$ -parametrization throughout the paper. Assume  $\boldsymbol{\theta} = (\theta_1, \dots, \theta_m) \in \mathcal{R}^m$ , which can always be obtained by ad-hoc transformations of each element of  $\boldsymbol{\theta}$ , we proceed as follows:

1. Find the mode  $\boldsymbol{\theta}^*$  of  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  and compute the negative Hessian  $\mathbf{H}$  at the modal configuration
2. Compute the eigen-decomposition  $\boldsymbol{\Sigma} = \mathbf{V}\boldsymbol{\Lambda}^{1/2}\mathbf{V}^T$  where  $\boldsymbol{\Sigma} = \mathbf{H}^{-1}$
3. Define a new  $\mathbf{z}$ -variable such that

$$\boldsymbol{\theta}(\mathbf{z}) = \boldsymbol{\theta}^* + \mathbf{V}\boldsymbol{\Lambda}^{1/2}\mathbf{z}$$

The variable  $\mathbf{z} = (z_1, \dots, z_m)$  is standardized and its components are mutually orthogonal.

At this point, if the dimension of  $\boldsymbol{\theta}$  is small, say  $m \leq 5$ , Rue et al. (2009) propose to use the  $\mathbf{z}$ -parametrization to build a grid covering the area where the density of  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  is higher. Such procedure has a computational cost which grows exponentially with  $m$ . It turns out that, when the goal is  $\pi(x_i|\mathbf{y})$ , a rather rough grid is enough to give accurate results.

If the dimension of  $\boldsymbol{\theta}$  is higher, Rue et al. (2009) propose a different approach, named CCD integration. Here the integration problem is considered as a design problem and, using the mode  $\boldsymbol{\theta}^*$  and the negative Hessian  $\mathbf{H}$  as a guide, we locate some “points” in the  $m$ -dimensional space which allows us to approximate the unknown function with a second order surface (see Section 6.5 of Rue et al., 2009). The CCD strategy requires much less computational power compared to the grid strategy but, when the goal is  $\pi(x_i|\mathbf{y})$ , it still allows to capture variability in the hyperparameter space when this is too wide to be explored via the grid strategy.

Figure 1 shows the location of the integration points in a two dimensional  $\boldsymbol{\theta}$ -space using the grid and the CCD strategy.

### 3.2 Algorithms for computing $\tilde{\pi}(\theta_j|\mathbf{y})$

If the dimension of  $\boldsymbol{\theta}$  is not too high, it is possible to evaluate  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  on a regular grid and use the resulting values to numerically compute the integral in Eq. (3) by summing out the variables  $\boldsymbol{\theta}_{-j}$ . Of course this is a naive solution in which the cost to obtain  $m$  such marginals would increase

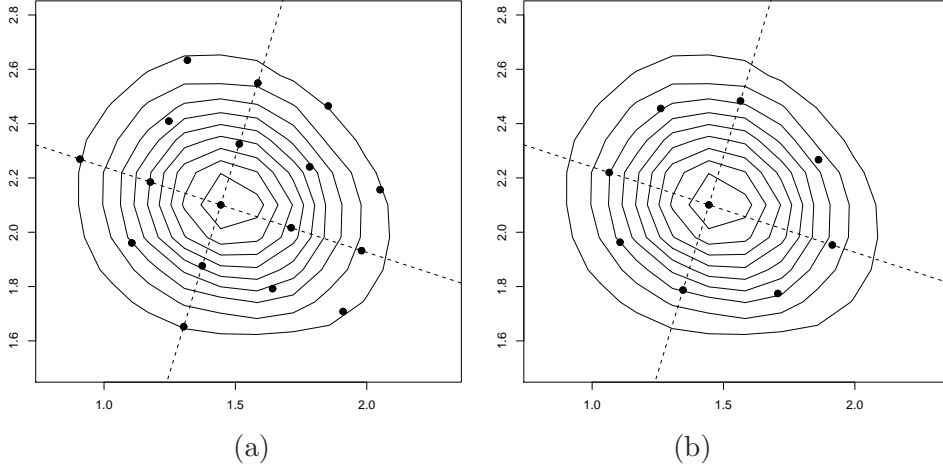


Figure 1: Location of the integration points in a two dimensional  $\boldsymbol{\theta}$ -space using the (a) grid and (b) the CCD strategy

exponentially on  $m$ . A more elaborate solution would be to use a Laplace approximation

$$\tilde{\pi}(\theta_j|\mathbf{y}) \approx \frac{\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})}{\tilde{\pi}_G(\boldsymbol{\theta}_{-j}|\theta_j, \mathbf{y})} \Big|_{\boldsymbol{\theta}_{-j}=\boldsymbol{\theta}_{-j}^*}. \quad (7)$$

where  $\boldsymbol{\theta}_{-j}^*$  is the modal configuration of  $\tilde{\pi}(\boldsymbol{\theta}_{-j}|\theta_j, \mathbf{y})$  and  $\tilde{\pi}_G(\boldsymbol{\theta}_{-j}|\theta_j, \mathbf{y})$  is a Gaussian approximation to  $\tilde{\pi}(\boldsymbol{\theta}_{-j}|\theta_j, \mathbf{y})$  built by matching the mode and the curvature at the mode. This would certainly give us accurate results but it requires to find the maximum of the  $(m-1)$  dimensional function  $\pi(\boldsymbol{\theta}_{-j}|\theta_j, \mathbf{y})$  for each value of  $\theta_j$ , which again does not scale well with the dimension  $m$  of the problem. Besides that, the Hessian computed at the numerically computed "mode" of  $\pi(\boldsymbol{\theta}_{-j}|\theta_j, \mathbf{y})$  was not always positive definite, which became a major issue. It is worth pointing out that in latent Gaussian models of interest, the dimension of the latent field is usually quite big, which makes the evaluation of  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  given by Eq. (5) expensive. With that in mind, it is useful to build and use algorithms that uses the density points already evaluated in the grid exploration of  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  as described in Section 3.1. Remember that those grid points already had to be computed in order to integrate out the uncertainty about  $\boldsymbol{\theta}$  using Eq. (2), so that algorithms that uses those points to compute the posterior marginals for  $\boldsymbol{\theta}$  would be doing so with little extra cost.

### 3.2.1 Asymmetric Gaussian interpolation

Some information about the marginals  $\pi(\theta_j|\mathbf{y})$  can be obtained by approximating the joint distribution  $\pi(\boldsymbol{\theta}|\mathbf{y})$  with a multivariate Normal distribution by matching the mode and the

curvature at the mode of  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$ . Such Gaussian approximation for  $\pi(\theta_j|\mathbf{y})$  comes with no extra computational effort since the mode  $\boldsymbol{\theta}^*$  and the negative Hessian  $\mathbf{H}$  of  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  are already computed in the numerical strategy used to approximate Eq. (2) as described in Section 3.1.

Unfortunately,  $\pi(\theta_j|\mathbf{y})$  can be rather skewed so that a Gaussian approximation is inaccurate. It is possible to correct the Gaussian approximation for the lack of asymmetry, with minimal additional costs, as described in the following.

Let  $\mathbf{z}(\boldsymbol{\theta}) = (z_1(\boldsymbol{\theta}), \dots, z_m(\boldsymbol{\theta}))$  be the point in the  $\mathbf{z}$ -parametrization corresponding to  $\boldsymbol{\theta}$ . We define the function  $f(\boldsymbol{\theta})$  as

$$f(\boldsymbol{\theta}) = \prod_{j=1}^m f_j(z_j(\boldsymbol{\theta})) \quad (8)$$

where

$$f_j(z) \propto \begin{cases} \exp\left(-\frac{1}{2(\sigma^{j+})^2}z^2\right) & \text{if } z \geq 0 \\ \exp\left(-\frac{1}{2(\sigma^{j-})^2}z^2\right) & \text{if } z < 0. \end{cases} \quad (9)$$

In order to capture some of the asymmetry of  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  we allow the scaling parameters  $(\sigma^{j+}, \sigma^{j-})$ ,  $j = 1, \dots, m$ , to vary not only according the  $m$  different axis but also according to the direction, positive and negative, of each axis. To compute these, we first note that in a Gaussian density, the drop in log density when we move from the mode to  $\pm 2$  the standard deviation is  $-2$ . We compute our scaling parameters in such a way that this is approximately true for all directions. We do this while exploring  $\tilde{\pi}(\boldsymbol{\theta}|\mathbf{y})$  to solve Eq. (2), meaning that no extra cost is required. An illustration of this process is given in Figure 2.

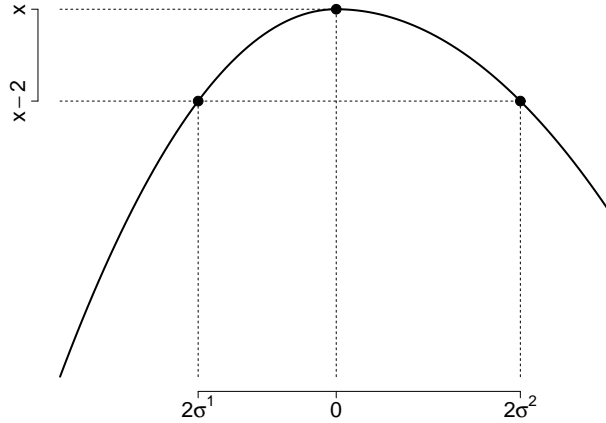


Figure 2: Schematic picture of the process to compute the scaling parameters that determine the form of the asymmetric Gaussian function given by Eq. (9). The solid line is the log-density of the distribution we want to approximate, and the scaling parameters  $\sigma^1$  and  $\sigma^2$  are obtained accordingly to a  $-2$  drop in the target log-density.

Approximations for  $\pi(\theta_j|\mathbf{y})$  are then computed via numerical integration of Eq. (8), which is easy to do once the scaling parameters are known. Figure 3 illustrates the flexibility of  $f_j(z)$  in Eq. (9) for different values of  $\sigma^-$  and  $\sigma^+$ .

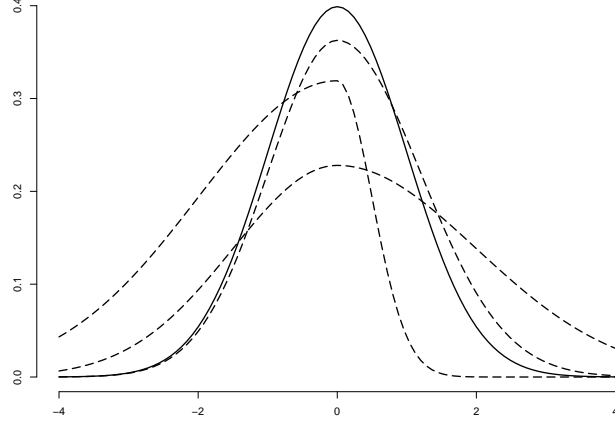


Figure 3: Standard normal distribution (solid line) and densities given by Eq. (9) for different values of the scaling parameters (dashed lines).

This algorithm was successfully used in the R-INLA package for a long time, and our experience is that it gives accurate results with low computational time. However, we came to realize that the multi-dimensional numerical integration algorithms available to integrate out  $\boldsymbol{\theta}_{-j}$  in Eq. (8) gets increasingly unstable as we start to fit models with higher number of hyperparameters, resulting in approximated posterior marginals densities with undesirable spikes instead of smooth ones. This has lead us to look for an algorithm that gives us accurate and fast approximations without the need to use those multi-dimensional integration algorithms, and we now describe our proposed solution.

### 3.2.2 Numerical integration free algorithm

The approximated posterior marginals  $\tilde{\pi}(\theta_j|\mathbf{y})$  returned by the new numerical integration free algorithm will assume the following structure,

$$\tilde{\pi}(\theta_j|\mathbf{y}) = \begin{cases} N(0, \sigma_{j+}^2), & \theta_j > 0 \\ N(0, \sigma_{j-}^2), & \theta_j \leq 0 \end{cases} \quad (10)$$

and the question now becomes how to compute  $\sigma_{j+}^2, \sigma_{j-}^2, j = 1, \dots, m$  without using numerical integration as in Section 3.2.1. The following lemma will be useful for that (Rue et al., 2009),

**Lemma 1.** Let  $\mathbf{x} = (x_1, \dots, x_n)^T \sim N(\mathbf{0}, \Sigma)$ ; then for all  $x_1$

$$-\frac{1}{2}(x_1, E(\mathbf{x}_{-1}|x_1)^T)\Sigma^{-1}\begin{pmatrix} x_1 \\ E(\mathbf{x}_{-1}|x_1) \end{pmatrix} = -\frac{1}{2}\frac{x_1^2}{\Sigma_{11}}$$

The lemma above can be used in our favor since it states that the joint distribution of  $\boldsymbol{\theta}$  as a function of  $\theta_i$  with  $\boldsymbol{\theta}_{-i}$  evaluated at the conditional mean  $E(\boldsymbol{\theta}_{-i}|\theta_i)$  behaves as the marginal of  $\theta_i$ . In our case this will be an approximation since  $\boldsymbol{\theta}$  is not Gaussian.

For each axis  $j = 1, \dots, m$  our algorithm will compute the conditional mean  $E(\boldsymbol{\theta}_{-j}|\theta_j)$  assuming  $\boldsymbol{\theta}$  to be Gaussian, which is linear in  $\theta_j$  and depend only on the mode  $\boldsymbol{\theta}^*$  and covariance  $\Sigma$  already computed in the grid exploration of Section 3.1, and then use Lemma 1 to explore the approximated posterior marginal of  $\theta_j$  in each direction of the axis. For each direction of the axis we only need to evaluate three points of this approximated marginal given by Lemma 1, which is enough to compute the second derivative and with that get the standard deviations  $\sigma_j^-$  and  $\sigma_j^+$  required to represent Eq. (10).

**Example 1.** To illustrate the difference in accuracy between the numerical integration free algorithm and the posterior marginals obtained via a more computationally intensive grid exploration we show in Figure 4 the posterior marginals of the hyperparameters of Example 3 computed by the first (solid line) and by the latter (dashed line). We can see that we lose accuracy when using the numerical integration free algorithm but it still gives us sensible results with almost no extra computation time while we need to perform a second finer grid exploration to obtain a more accurate result via the grid method, a operation that can take a long time in examples with high dimension of the latent field and/or hyperparameters. The numerical integration free algorithm is the default method to compute the posterior marginals for the hyperparameters. In order to get more accurate results via the grid method the user needs to use the output of the `inla` function into the `inla.hyperpar` function. For example, to generate the marginals computed by the grid method in Figure 4 we have used

```
result.hyperpar = inla.hyperpar(result)
```

The asymmetric Gaussian interpolation can still be used through the `control.inla` argument:

```
inla(..., control.inla = list(interpolator = "ccdintegrate"), ...)
```

## 4 Extending the scope of INLA

This section formalizes several features available within the R-INLA package that greatly extend the scope of models available through that interface. The features are illustrated with small

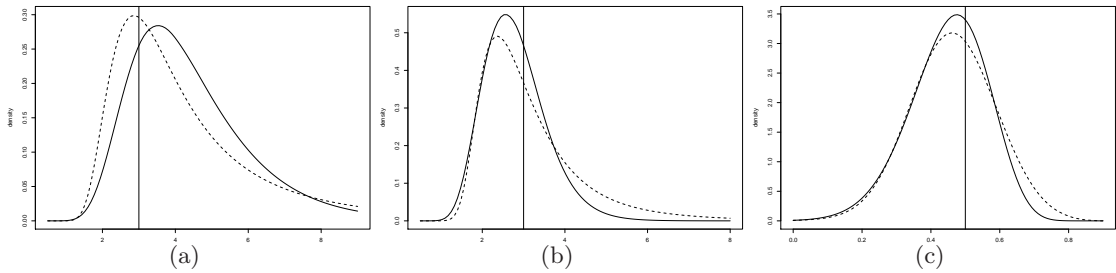


Figure 4: Posterior distribution for the hyperparameters in the replicate example with a vertical line to indicate the true values used in the simulation. Solid line computed by the numerical integration free algorithm and dashed line computed via the more expensive grid exploration. (a) Gaussian observational precision (b) Precision of the AR(1) latent model (c) persistence parameter for the AR(1) process

examples that help to understand the usefulness of the features and to apply it through **R** code available along the paper.

#### 4.1 Multiple likelihoods

In many applications, different subsets of data may have been generated by different sources, leading us to be interested in models where each subset of data may be described by a different likelihood function. Here different likelihood functions might mean either a different family of distribution, as for example when a subset of the data follow a Gaussian distribution and the other follow a Poisson distribution or, the same family of distribution but with different hyperparameters, as for example when one subset of the data comes from a Gaussian distribution with unknown precision  $\tau_1$  and the other from a Gaussian with unknown precision  $\tau_2$ . Concrete examples of the usefulness of this feature can be found in Guo and Carlin (2004) where longitudinal and event time data are jointly modeled or in the preferential sampling framework of Diggle et al. (2010) where geostatistical models with stochastic dependence between the continuous measurements and the locations at which the measurements were made are presented. **R** code for the examples presented at those papers can be found at the case studies section at the INLA website.

Although being a very useful feature, models with multiple likelihoods are not straightforward, if at all possible, to implement through many of the popular packages available in **R**. From a theoretical point of view there is nothing that keep us from fitting a model with multiple likelihoods with the INLA approach. The only requirements, as described in Section 2.1, are that the likelihood function must have conditional independence properties given the latent field

$\mathbf{x}$  and hyperparameters  $\boldsymbol{\theta}_1$ , and that each data-point  $y_i$  must be connected to one element in the latent field  $x_i$ , so that

$$\pi(\mathbf{y}|\mathbf{x}, \boldsymbol{\theta}_1) = \prod_{i=1}^{n_d} \pi(y_i|x_i, \boldsymbol{\theta}_1).$$

Even this last restriction will be made more flexible in Section 4.5 where each data-point  $y_i$  may be connected with a linear combination of the elements in the latent field.

Models with multiple likelihoods can be fitted through the R-INLA package by rewriting the response variable as a matrix (or list) where the number of columns (or elements in the list) are equal to the number of different likelihood functions. The following small example will help to illustrate the process.

**Example 2.** Suppose we have a dataset  $\mathbf{y}$  with  $2n$  elements where the first  $n$  data points come from a binomial experiment and the last  $n$  data points come from a Poisson distribution. In this case the response variable to be used as input to the `inla()` function must be written as a matrix with two columns and  $2n$  rows where the first  $n$  elements of the first column hold the binomial data while the last  $n$  elements of the second column hold the Poisson data, and all other elements of the matrix should be filled with NA. Following is R code to simulate data following the description above together with R-INLA code to fit the appropriate model to the simulated data.

```
n = 100
x1 = runif(n)
eta1 = 1 + x1
y1 = rbinom(n, size = 1, prob = exp(eta1)/(1+exp(eta1))) # binomial data
x2 = runif(n)
eta2 = 1 + x2
y2 = rpois(n, exp(eta2))
Y = matrix(NA, 2*n, 2) # need the response variable as matrix
Y[1:n, 1] = y1          # binomial data
Y[1:n + n, 2] = y2      # poisson data
Ntrials = c(rep(1,n), rep(NA, n)) # required only for binomial data
xx = c(x1, x2)
formula = Y ~ 1 + xx
result = inla(formula, data = list(Y = Y, xx = xx),
              family = c("binomial", "poisson"), Ntrials = Ntrials)
summary(result)
plot(result)
```



## 4.2 Replicate feature

The replicate feature in R-INLA allows us to define models where the latent field  $\mathbf{x}$  contain conditional independent replications of the same latent model given some hyperparameters. Assume for example that  $\mathbf{z}_1$  and  $\mathbf{z}_2$  are independent replications from  $\mathbf{z}|\boldsymbol{\theta}$  such that  $\mathbf{x} = (\mathbf{z}_1, \mathbf{z}_2)$  and

$$\pi(\mathbf{x}|\boldsymbol{\theta}) = \pi(\mathbf{z}_1|\boldsymbol{\theta})\pi(\mathbf{z}_2|\boldsymbol{\theta}) \quad (11)$$

It is important to note here that although the process  $\mathbf{z}_1$  and  $\mathbf{z}_2$  are conditionally independent given  $\boldsymbol{\theta}$  they both convey information about  $\boldsymbol{\theta}$ . A latent model such as (11) can be defined in the R-INLA package using the `replicate` argument inside the `f()` function used to specify the random effect components as described in Section 2.3.

**Example 3.** Let us define the following  $AR(1)$  process

$$x_1 \sim N(0, (\kappa(1 - \phi^2))^{-1})$$

$$x_i = \phi x_{i-1} + \epsilon_i; \quad \epsilon_i \sim N(0, \kappa^{-1}), \quad i = 2, \dots, n$$

with  $\phi$  and  $\kappa$  being unknown hyperparameters satisfying  $|\phi| < 1$  and  $\kappa > 0$ . Denote by  $\tau$  the marginal precision of the process,  $\tau = \kappa(1 - \phi^2)$ . Now assume two conditionally independent realizations  $\mathbf{z}_1$  and  $\mathbf{z}_2$  of the  $AR(1)$  process defined above given the hyperparameters  $\boldsymbol{\theta} = (\phi, \tau)$ . We are then given a dataset  $\mathbf{y}$  with  $2n$  elements where the first  $n$  elements come from a Poisson with intensity parameters given by  $\exp(\mathbf{z}_1)$  and the last  $n$  elements of the dataset come from a Gaussian with mean  $\mathbf{z}_2$ . The latent model  $\mathbf{x} = (\mathbf{z}_1, \mathbf{z}_2)$  described here can be specified with a two dimensional index  $(i, r)$  where  $i$  is the position index for each process and  $r$  is the index to label the process. Following is the INLA code to fit the model we just described to simulated data with  $\phi = 0.5$ ,  $\kappa = \sqrt{2}$  and Gaussian observational precision  $\tau_{obs} = 3$ . Priors for the hyperparameters were chosen following the guide-lines described in Fong et al. (2010). Figure 5 show the simulated  $\mathbf{z} = (\mathbf{z}_1, \mathbf{z}_2)$  (solid line) together with posterior means and (0.025, 0.975)-quantiles (dashed line) returned by INLA. Figure 6 show the posterior distributions for the hyperparameters returned by INLA with a vertical line to indicate true values used in the simulation.

```
n = 100
z1 = arima.sim(n, model = list(ar = 0.5), sd = 0.5) # independent replication
z2 = arima.sim(n, model = list(ar = 0.5), sd = 0.5) # from AR(1) process
y1 = rpois(n, exp(z1))
y2 = rnorm(n, mean = z2, sd = 1/sqrt(3))
y = matrix(NA, 2*n, 2) # Setting up matrix due to multiple likelihoods
y[1:n, 1] = y1
```

```

y[n + 1:n, 2] = y2
hyper.gaussian = list(prec = list(prior = "loggamma",      # prior for Gaussian
                                param = c(1, 0.2161))) # likelihood precision
hyper.ar1 = list(prec = list(prior = "loggamma",          # priors for the
                            param = c(1, 0.2161)),       # 'ar1' model
                rho = list(prior = "normal",
                           param = c(0, 0.3)))

i = rep(1:n, 2)      # position index for each process
r = rep(1:2, each = n) # index to label the process
formula = y ~ f(i, model = "ar1", replicate = r, hyper = hyper.ar1) -1
result = inla(formula, family = c("poisson", "gaussian"),
              data = list(y = y, i = i, r = r),
              control.family = list(list(), list(hyper = hyper.gaussian)))

summary(result)
plot(result)

```

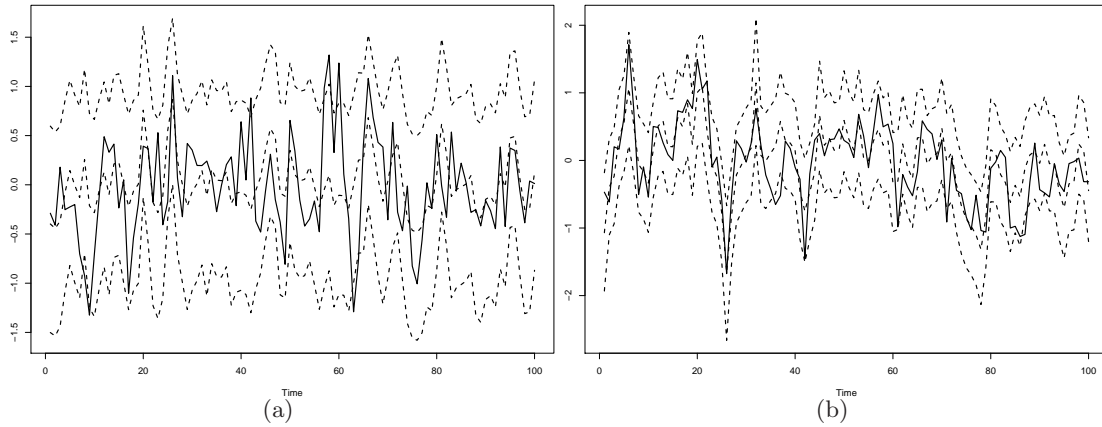


Figure 5: Replicate example: (a) Simulated  $z_1$  process (solid line) together with posterior means and (0.025, 0.975) quantiles returned by INLA (dashed line) (b) Simulated  $z_2$  process (solid line) together with posterior means and (0.025, 0.975) quantiles returned by INLA (dashed line)

□

### 4.3 Copy feature

The `formula` syntax as illustrated in Section 2.3 allow us to have only one element from each latent model to contribute to the linear prediction specification. So that a model formulation such as

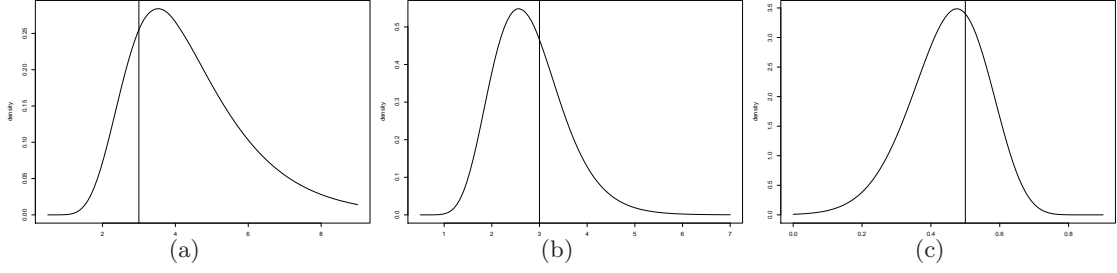


Figure 6: Posterior distribution for the hyperparameters in the replicate example with a vertical line to indicate the true values used in the simulation. (a) Gaussian observational precision (b) Precision of the AR(1) latent model (c) lag-one correlation for the AR(1) process

```
formula = y ~ f(idx1, model1, ...) + f(idx2, model2, ...)
```

indicate that each data point  $y_i$  is connected to one linear predictor  $\eta_i$  through a given link function  $g$  and that each  $\eta_i$  is connected to one element of the random effect `idx1` and to one element of the random effect `idx2`. Unfortunately this is not always enough as illustrated in the example below.

**Example 4.** Suppose our data come from a Gaussian distribution  $y_i \sim N(\eta_i, \tau^{-1})$ ,  $i = 1, \dots, n$ , where the linear prediction  $\eta_i$  assume the following form

$$\eta_i = a_i + b_i z_i, \quad (a_i, b_i) \stackrel{iid}{\sim} N_2(0, \mathbf{Q}^{-1}),$$

where  $\mathbf{z}$  represent here known covariates. The bi-variate Gaussian model  $N_2(0, \mathbf{Q}^{-1})$  is defined in R-INLA by `f(i, model = "iid2d")`. However, a definition like

```
formula = y ~ f(i, model = "iid2d", ...) - 1
```

does not allow us to define the model of interest where each linear predictor  $\eta_i$  is connected to two elements of the bi-variate Gaussian model, which are  $a_i$  and  $b_i$  in this case. To address this inconvenience the `copy` feature was created and our model formulation could be defined by

```
formula = y ~ f(i, model = "iid2d", n = 2*n) +  
          f(i.plus, z, copy = "i")
```

with appropriate definitions for the indexes `i` and `i.plus`. The `copy` feature is not limited to the bivariate case as in the above example, we could easily have defined a model where each linear predictor is connected to three or more elements of a given latent model. For example, if we had a trivariate Gaussian

$$\eta_i = a_i + b_i z_{1,i} + c_i z_{2,i}, \quad (a_i, b_i, c_i) \stackrel{iid}{\sim} N_3(0, \mathbf{Q}^{-1}),$$

we would use

```
formula = y ~ f(i, model = "iid3d", n = 3*n) +
          f(i.plus1, z1, copy = "i") +
          f(i.plus2, z2, copy = "i")
```

with appropriate definitions for the indexes `i`, `i.plus1` and `i.plus2`.

Below is R code to simulate data and to fit the bivariate model described above with INLA. The data is simulated with observational precision  $\tau = 1$  and bi-variate Gaussian distribution for the random-effects  $(a_i, b_i)$ ,  $i = 1, \dots, 1000$  with marginal precisions  $\tau_a = \tau_b = 1$  for  $a_i$  and  $b_i$  respectively, and correlation  $\rho_{ab}$  between  $a_i$  and  $b_i$  equal to 0.8. Figure 7 show the posterior marginals for the hyperparameters returned by INLA.

```
n = 1000
Sigma = matrix(c(1, 0.8, 0.8, 1), 2, 2)
z = rnorm(n)
ab = rmvnorm(n, sigma = Sigma) # require 'mvtnorm' package
a = ab[, 1]
b = ab[, 2]
eta = a + b * z
y = eta + rnorm(n, sd = 1)
hyper.gaussian = list(prec = list(prior = "loggamma",
                                   param = c(1, 0.2161)))

i = 1:n      # use only the first n elements (a_1, ..., a_n)
j = 1:n + n # use only the last n elements (b_1, ..., b_n)
formula = y ~ f(i, model = "iid2d", n = 2*n) +
          f(j, z, copy = "i") - 1
result = inla(formula, data = list(y = y, z = z, i = i, j = j),
              family = "gaussian",
              control.data = list(hyper = hyper.gaussian))
summary(result)
plot(result)
```

□

Formally, the copy feature is used when a latent field is needed more than once in the model formulation. When using the feature we then create a (almost) identical copy of  $\mathbf{x}_S$ , denoted here by  $\mathbf{x}_S^*$ , that can then be used in the model formulation as shown in Example 4. In this

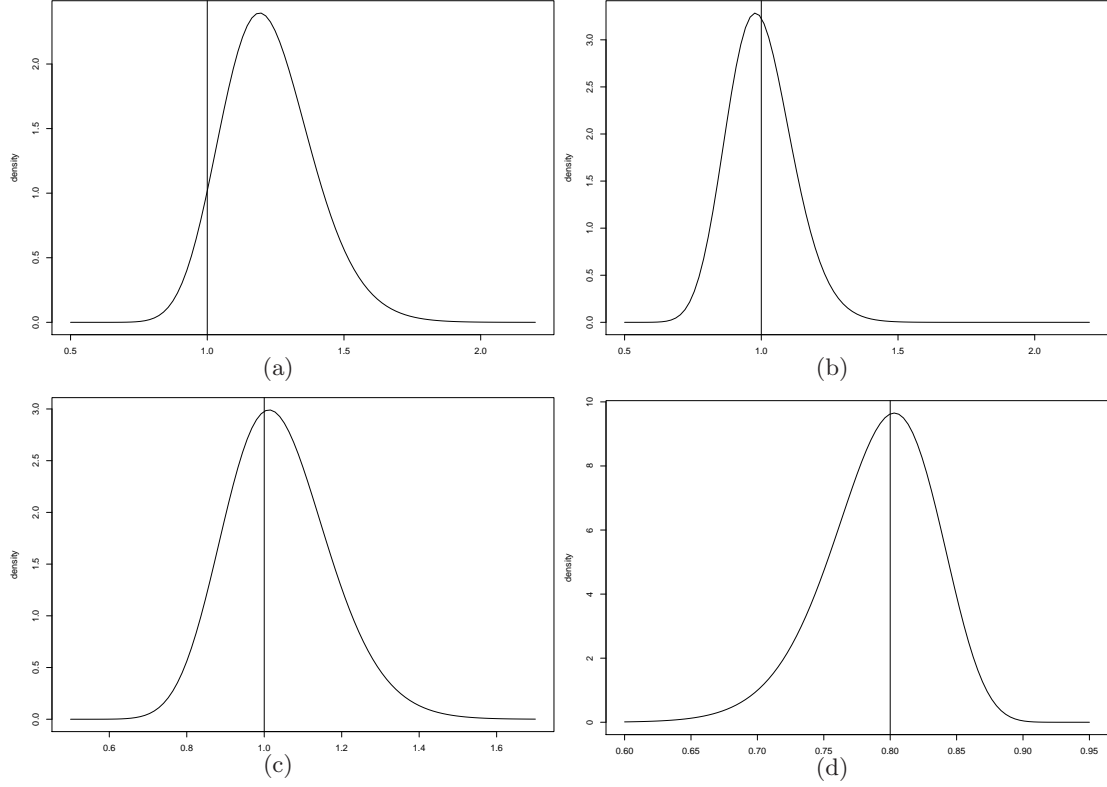


Figure 7: Posterior distribution for the hyperparameters in the copy example with a vertical line to indicate the true values used in the simulation. (a) Gaussian observational precision  $\tau$  (b) Marginal precision for  $a_i$ ,  $\tau_a$  (c) Marginal precision for  $b_i$ ,  $\tau_b$  (d) Correlation between  $a_i$  and  $b_i$ ,  $\rho_{ab}$ .

case, we have extended our latent field from  $\mathbf{x}_S$  to  $\mathbf{x} = (\mathbf{x}_S, \mathbf{x}_S^*)$ , where  $\pi(\mathbf{x}) = \pi(\mathbf{x}_S)\pi(\mathbf{x}_S^*|\mathbf{x}_S)$  and

$$\pi(\mathbf{x}_S^*|\mathbf{x}_S, \tau) \propto \exp \left\{ \frac{-\tau}{2} (\mathbf{x}_S^* - \mathbf{x}_S)^T (\mathbf{x}_S^* - \mathbf{x}_S) \right\} \quad (12)$$

so that the degree of closeness between  $\mathbf{x}_S$  and  $\mathbf{x}_S^*$  is controlled by the fixed high precision  $\tau$  in Eq. (12), which has a default value of  $\tau = \exp 15$ . It is also possible for the copied model to have an unknown scale parameter  $\psi$ , in which case

$$\pi(\mathbf{x}_S^*|\mathbf{x}_S, \tau, \psi) \propto \exp \left\{ \frac{-\tau}{2} (\mathbf{x}_S^* - \psi \mathbf{x}_S)^T (\mathbf{x}_S^* - \psi \mathbf{x}_S) \right\}. \quad (13)$$

#### 4.4 Linear combinations of the latent field

Depending on the context, interest might lie not only on posterior marginals of the elements in the latent field but also on linear combinations of those elements. Assume  $\mathbf{v}$  are the linear

combinations of interest, it can then be written as

$$\mathbf{v} = \mathbf{B}\mathbf{x},$$

where  $\mathbf{x}$  is the latent field and  $\mathbf{B}$  is a  $k \times n$  matrix where  $k$  is the number of linear combinations and  $n$  is the size of the latent field. The functions `inla.make.lincomb` and `inla.make.lincombs` in R-INLA are used to define a linear combination and many linear combinations at once, respectively.

R-INLA provides two approaches for dealing with  $\mathbf{v}$ . The first approach creates an enlarged latent field  $\tilde{\mathbf{x}} = (\mathbf{x}, \mathbf{v})$  and then use the INLA method as usual to fit the enlarged model. After completion we then have posterior marginals for each element of  $\tilde{\mathbf{x}}$  which includes the linear combinations  $\mathbf{v}$ . Using this approach the marginals can be computed using the Gaussian, Laplace or simplified Laplace approximations discussed in Section 2.2. The drawback is that the addition of many linear combinations will lead to more dense precision matrices which will consequently slow down the computations. This approach can be used by defining the linear combinations of interest using the functions mentioned on the previous paragraph and using `control.inla = list(lincomb.derived.only = FALSE)` as an argument to the `inla` function.

The second approach does not include  $\mathbf{v}$  in the latent field but perform a post-processing of the resulting output given by INLA and approximate  $\mathbf{v}|\boldsymbol{\theta}, \mathbf{y}$  by a Gaussian where

$$\mathbb{E}_{\mathbf{v}|\boldsymbol{\theta}, \mathbf{y}}(\mathbf{v}) = \mathbf{B}\boldsymbol{\mu}^* \quad \text{and} \quad \text{Var}_{\mathbf{v}|\boldsymbol{\theta}, \mathbf{y}}(\mathbf{v}) = \mathbf{B}\mathbf{Q}^{*-1}\mathbf{B}^T,$$

in which  $\boldsymbol{\mu}^*$  is the mean of best marginal approximation used for  $\pi(x_i|\boldsymbol{\theta}, \mathbf{y})$  (i.e. Gaussian, Simplified Laplace or Laplace approximation) and  $\mathbf{Q}^*$  is the precision matrix of the Gaussian approximation  $\pi_G(\mathbf{x}|\boldsymbol{\theta}, \mathbf{y})$  used in Eq. (5). Then approximation for the posterior marginals of  $\mathbf{v}$  are obtained by integrating  $\boldsymbol{\theta}$  out in a process similar to Eq. (2). The advantage here is that the computation of the posterior marginals for  $\mathbf{v}$  does not affect the graph of the latent field, leading to a much faster approximation. That is why this is the default method in R-INLA, but more accurate approximations can be obtained by switching to the first approach, if necessary.

**Example 5.** Following is R code to compute the posterior marginal of a linear combination between elements of the  $AR(1)$  process of Example 3. More specifically, we are interested in

$$v_1 = 3z_{1,2} - 5z_{1,4}$$

$$v_2 = z_{1,3} + 2z_{1,5},$$

where  $z_{i,j}$  denote the  $j$ th element of the latent model  $\mathbf{z}_i$  as defined in Example 3.

```

# define the linear combinations:
# v_1 = 3*z_{1,2} - 5*z_{1,4}
# v_2 = z_{1,3} + 2*z_{1,5}
lc1 = inla.make.lincomb(i = c(NA, 3, NA, -5))
names(lc1) = "lc1"
lc2 = inla.make.lincomb(i = c(NA, NA, 1, NA, 2))
names(lc2) = "lc2"
# compute v_1 and v_2 using the default method.
result = inla(formula,
               family = c("poisson", "gaussian"),
               data = list(y = y, i = i, r = r),
               control.family = list(list(), list(hyper = hyper.gaussian)),
               lincomb = c(lc1, lc2))

# compute v_1 and v_2 with the more accurate (and slow) approach.
result2 = inla(formula,
                family = c("poisson", "gaussian"),
                data = list(y = y, i = i, r = r),
                control.family = list(list(), list(hyper = hyper.gaussian)),
                lincomb = c(lc1, lc2),
                control.inla = list(lincomb.derived.only = FALSE))

```

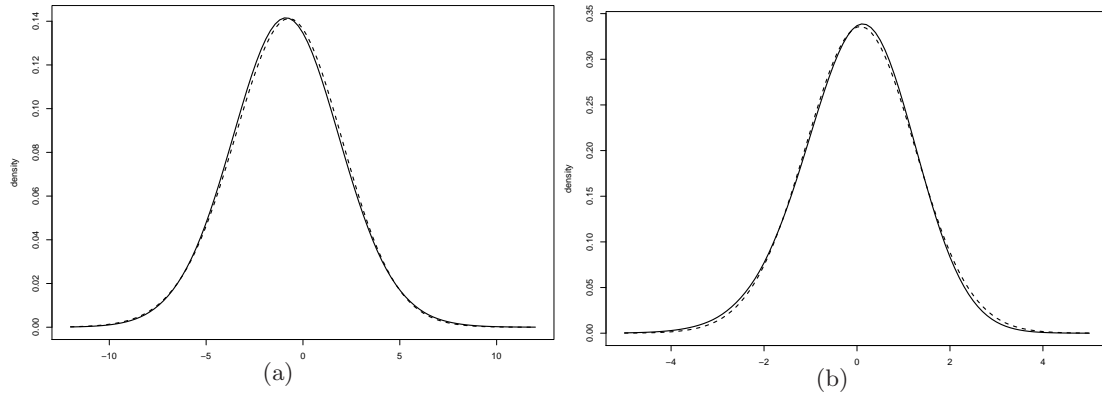


Figure 8: Posterior distribution for the linear combinations computed with both methods described in Section 4.4, the solid line represent the more accurate approach while the dashed line represent the faster one. (a) Posterior distribution for  $v_1$  (b) Posterior distribution for  $v_2$ .

The code illustrates how to use both approaches described in this section and Figure 8 shows the posterior distributions for  $v_1$  and  $v_2$  computed with the more accurate approach (solid line) and with the faster one (dashed line). We can see little difference between the two approaches

in this example. We refer to the **FAQ** section on the **R-INLA** website for more information about defining multiple linear combinations at once.

□

When using the faster approach, there is also an option to compute the posterior correlation matrix between all the linear combinations by using

```
control.inla = list(lincomb.derived.correlation.matrix = TRUE)
```

This correlation matrix could be used for example to build a Gaussian copula to approximate the joint density of some components of the latent field, as discussed in Section 6.1 of Rue et al. (2009).

#### 4.5 More flexible dependence on the latent field

As mentioned in Section 2.1, the INLA method in its original implementation allowed each data point to be connected to only one element in the latent field. While this is often the case, this assumption is violated, for example, when the observed data consists of area or time averages of the latent field. In this case,

$$y_i | \mathbf{x}, \boldsymbol{\theta}_1 \sim \pi(y_i | \sum_j a_{ij} x_j, \boldsymbol{\theta}_1). \quad (14)$$

Assume  $\mathbf{A}$  to be the matrix formed by the  $\{a_{ij}\}$  elements in Eq. (14). We further assume that the dependence of the data on the latent field is “local” in the sense that most elements of  $\mathbf{A}$  are zero. With this assumption everything stays Markovian and fast inference is still possible. This is defined in **R-INLA** by modifying the `control.compute` argument of the `inla` function as follows:

```
inla(..., control.compute = list(A = A))
```

Internally, **R-INLA** add another layer in the hierarchical model

$$\boldsymbol{\eta}^* = \mathbf{A}\boldsymbol{\eta}$$

where  $\boldsymbol{\eta}^*$  is formed by a linear combination of the linear predictor  $\boldsymbol{\eta}$ , but now the likelihood function is connected to the latent field through  $\boldsymbol{\eta}^*$  instead of  $\boldsymbol{\eta}$ ,

$$\mathbf{y} | \mathbf{x}, \boldsymbol{\theta}_1 \sim \prod_{i=1}^{n_d} \pi(y_i | \eta_i^*, \boldsymbol{\theta}_1).$$



This is a very powerful feature that allow us to fit models with a likelihood representation given by Eq. (14) and besides it can even mimic to some extent the copy feature of Section 4.3, with the exception that the copy feature allow us to copy model components using an unknown scale parameter as illustrated in Eq. (13). This feature is implemented by also adding  $\boldsymbol{\eta}^*$  to the latent model, where the conditional distribution for  $\boldsymbol{\eta}^*$  has mean  $\mathbf{A}\boldsymbol{\eta}$  and precision matrix  $\kappa_A \mathbf{I}$  where the constant  $\kappa_A$  is set to a high value, like  $\kappa_A = \exp(15)$  a priori. In terms of output from `inla`, then  $(\boldsymbol{\eta}^*, \boldsymbol{\eta})$  is the linear predictor.

To illustrate the relation between the  $\mathbf{A}$  matrix and the copy feature we fit the model of Example 4 again but now using the feature described in this Section. Following is the R code:

```
## This is an alternative implementation of the model in Example 3
i = 1:(2*n)
zz = c(rep(1, n), z)
formula = y ~ f(i, zz, model = "iid2d", n = 2*n) - 1 # Define eta
I = Diagonal(n)
A = cBind(I,I) # Define A matrix used to construct eta* = A eta
result = inla(formula,
               data = list(y = y, zz = zz, i = i),
               family = "gaussian",
               control.predictor = list(A = A))
summary(result)
plot(result)
```

Although this  $\mathbf{A}$ -matrix feature can replicate the copy feature to some extent (remember that copy allow us to copy components with unknown scale parameters), for some models it is much simpler to use the copy feature. Which one is easier to use varies on a case-by-case basis and are left to the user to decide which one he or she is most comfortable with.

In some cases it has shown useful to simply *define* the model using the  $\mathbf{A}$ -matrix, by simply defining  $\boldsymbol{\eta}$  as a long vector of all the different components that the full model consist at, and then putting it all together using the  $\mathbf{A}$  matrix. The following simplistic linear regression example demonstrate the idea. Note that  $\eta_1$  is the intercept and  $\eta_2$  is the effect of covariate  $x$ .

```
n = 100
x = rnorm(n)
y = 1 + x + rnorm(n, sd = 0.1)
intercept = c(1, NA)
b = c(NA, 1)
A = cbind(1,x)
r = inla(y ~ -1 + intercept + b, family = "gaussian",
```

```
data = list(A = A, y = y, intercept = intercept, b = b),
control.predictor = list(A = A))
```

## 4.6 Kronecker feature

In a number of applications, the precision matrix in the latent model can be written as a Kronecker product of two precision matrices. A simple example of this is the separable space-time model constructed by using spatially correlated innovations in an  $AR(1)$  model:

$$\mathbf{x}_{t+1} = \phi \mathbf{x}_t + \boldsymbol{\epsilon}_t,$$

where  $\phi$  is a scalar and  $\boldsymbol{\epsilon} \sim N(0, \mathbf{Q}_\epsilon^{-1})$ . In this case the precision matrix is  $\mathbf{Q} = \mathbf{Q}_{AR(1)} \otimes \mathbf{Q}_\epsilon$ , where  $\otimes$  is the Kronecker product.

The general Kronecker product mechanism is currently in progress, but a number of special cases are already available in the code through the `group` feature. For example, a separable spatio-temporal model can be constructed using the command

```
result = y ~ f(loc, model = "besag",
               group = time, control.group = list(model = "ar1"))
```

in which every observation is assigned a location `loc` and a time `time`. At each time the points are spatially correlated while across the time periods, they evolve according to an  $AR(1)$  process; see for example Cameletti et al. (2012). Besides the  $AR(1)$  model, an uniform correlation matrix defining exchangeable latent models, a random-walk of order one (RW1) and of order two (RW2) are also implemented in R-INLA through the `group` feature.

## 5 Conclusion

The INLA framework has become a daily tool for many applied researchers from different areas of application. With this increase in usage came as well an increase in demand for the possibility to fit more complex models from within R. It has happened in a way that many of the latest developments have come from necessity expressed by the users. In this paper we have described and illustrated several new features implemented in the R package R-INLA that have greatly extended the scope of models available to be used within R. This is an active project that continues to evolve in order to fulfill, as well as possible, the demands of the statistical and applied community. Several case studies that have used the features formalized in this paper can be found in the INLA website. Those case studies treat a variety of situations, as for example dynamic models, shared random-effects models, spatio-temporal models and preferential sampling, and serve to illustrate the generic nature of the features presented in Section 4.

Most of the attention in Rue et al. (2009) have been focused on the algorithms to compute the posterior marginals of the latent field since this is usually the most challenging task given the usual big size of the latent field. However, the computation of posterior marginals of the hyperparameters is not straightforward given the high cost to evaluate the approximation to the joint density of hyperparameters. We have here described two algorithms that have been used successfully to obtain posterior marginals of the hyperparameters by using the few evaluation points already computed when integrating out the uncertainty with respect to the hyperparameters in the computation of the posterior marginals of the elements in the latent field.

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